pine.pair

GAP of: x69822.gb_pl   check: 4491   from: 1   to: 1423

```
LOCUS       PSGLN              1423 bp    mRNA      linear    PLN 30-SEP-1993
DEFINITION  P.sylvestris mRNA for glutamine synthetase.
ACCESION    X69822
VERSION     X69822.1   GI:404326
KEYWORDS    gln gene; glutamate-ammonia ligase; glutamine synthetase.
SOURCE      Pinus sylvestris (Scots pine)
```

to: m20663.gb_pl   check: 9167   from: 1   to: 1434

```
LOCUS       PEAGSCY1A          1434 bp    mRNA      linear    PLN 27-APR-1993
DEFINITION  Pisum sativum glutamine synthetase (cytosolic GS1) mRNA, complete
            cds.
ACCESION    M20663 J03878
VERSION     M20663.1   GI:169095
KEYWORDS    glutamine synthetase (cytosolic GS1).
```

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760

```
        Gap Weight:        1        Average Match:    10.000
     Length Weight:        0        Average Mismatch:  0.000

            Quality:   10444        Length:    1571
              Ratio:   7.339        Gaps:       166
Percent Similarity: 82.504     Percent Identity: 82.504
```

Match display thresholds for the alignment(s):
```
              | = IDENTITY
              ; = 5
              . = 1
```

x69822.gb_pl x m20663.gb_pl November 25, 2003 14:18

```
   1 .....T....TC.........C..CTTCC.....TC.....TGGTTTGTTTT  22
     1 CGCATAGAAATCTGAGGATTCATCATCCAAGGATCCACAGTGATTCAATTT  50

  23 GGAGAGTGGC......CATGTCGAGCGTATT...AA.CA.GAC.CT.....  56
     51 .CA.AGTTTTCTTTTTC.T.TC.A.CTTTTTCAAAACCATGTCTCTTTCA  94

  57 ....TC.TCAACCTTGA.C.CTGAGCG.ACGTGACGAGGAGGTCATTGC  98
     95 GATCTCATCAACCTTGATCTCTCAG.GAAC..CACCGAGAAAATCATAGC 141

  99 AGAGTATATATGGAGGATCAGGAATGGA.TATGCCGCAGT..AAAG 145
    142 AGAATACATATGGATTGGTGGTTCTTTGGGACT.TGAG..GTGCAAAG 188

 146 CCA.GATCTCTGT.CAGGACCTGTGAGT.AGCGGTAAAGAGCTTCCCAAA 192
    189 CAAGGA.CTCT.TCCCGGACCAGTTACTGACCCTT.CAGAGCTCCCCAAG 235

 193 TGGAACTATGACGGCTCCGCGACTGGACACGGCTCAAGGACATGACAGCGA 242
    236 TGGAATTATGATGGTTCCATGAGGCTGGACAAGGATCTGGACAAGATAGTGA 285

 243 AGTCAT.TCTATATCCACAAGCTA.TCTTCCGTGATCCATTTC.GCAGAG 289
    286 AGTTATCT.TATACCCACAAGCCATTTTAAG.GATCCA.TTCAGAAGGG 332

 290 GAAAGCACAT.T.TGGTAATCTGTGATGCCTACTCTCCTAATGG.G.AC 335
    333 GTAA.C.CATATCTTGGTTATGTGTGATGCATACAGTCCTGCTGGAGAAC 380

 336 TGCTATTCCTTC.C.AACAAGAGGGC.TGCAGCAGCGGAAATTTTTAACG 382
    381 ..CAATTCC..CACTAACAA.AAGCACACGCAGCTGCTAAGGTTTTTAGC. 424

 383 AAAAGGC.G..GTTAG.TGATGAAGAGAGACATGGTACGGGCT.T.GAACA 426
```

```
 425 ..CATCCTGATGTT.GTTGCTGAAGAAACATGGTATGG..TATAGAGCAG 469
     427 GAATATACAC.TGTTGCA.AAAGGACGTCAAATGCCTCTTGGCTGGCCA 474

 470 GAATACAC.CTTGTTGCAGAAA.GACATCAATGGCCTCTTGGTTGGCCA 517
     475 ATTGGGGGCTACCCGGTCCTCAGGGCCCCATATACTGTG...GAGTTGGA 522

 518 GCTGGGTGGTTATCCTGGACCTCAGGGACCATATTA.T.TGCAGTGTTGGT 565
     523 GCTGACAAAGCCTGGGGAGGACGAGACATTGTTGATGCCCATTATAAGGCTTG 572

 566 GCTGACAAGGCTTTGGCCGTGACGTTGTTGAGGCACATTACAAAGCCTG 615
     573 TCTCTATT.CAGGAATCAATATCAGTGGCATCAATGGAGAAGTCATGCCA 621

 616 TCT.TTTTGCCGGCATCAACATCAGTGAATCAATGGAGAAGTCATGCCT 664
     622 GGGCAGTGGGAATTCAAGTAGGTCCGTCAGTGGGTATCTCAGCAGCAGA 671

 665 GGTCAATGGGAATTTCAAGTGGGTCCCTCAGTCCGTATCCTCTGCTGGTGA 714
     672 TGAGCTGT.GGTGTGCTCGTTTTATTATGGAGGAGGATTACAGAAAAG..G 718

 715 TGAGATATGGGT.TGCTCCGCTACATTTTGGAGGAGGATCACTG..AGGTTG 761
     719 CGGGTGTCGTTCTGT.CCTTTGATCCC.AAGCCAATTGAGGGGGACTGGA 766

 762 CTGGTGTGGTTCT.TACCTTGA.CCCTAAACCAATTAAGGGTGGACTGGA 809
     767 ATGGTGCTGGATGC.CACACAAATACAGCACCAAGTCCATGGGCCA.AGG 814

 810 ATGGGGCTGG.TGCTCACACAACTACACAGCACCAAGTCATGAG.AGAAG 857
     815 AGGGAGGGCT.TCGAAGTAATTGAAGAAAGCAATAGAAAAAACT...GAAGTT 860

 858 ACGGTGGATAT.GAAATCATCAAGAAAGCAATTGAGAAGCTCGGAA... 903
     861 GAGAGGCATAAG...GAGCATATTTCTGCCTATGGGGAGGGAAATGAGAG.A 906

 904 GAGGC.T..GCCCGGACGACATCTCCGCTTATGGAGAAGCAAGCAGCCCA 950
     907 CGGCCTCACTGGTCG..GCACGAGACAGCAGCAAGAATACCTTTCCTGG 954

 951 .GATTGACAGG..GAAAACGGAAACAGCTGACATTAATACCTTCTCATCG 997
     955 GGTGTTGCAAATCGAGGAGCTTCAGTTAGAGTCCGGGACCACAGAAAA 1004

 998 GGTGTTGCAAACCGAGGGCCTTCGGTTCGGGTTGGAAGGGACCACAGAGA 1047
    1005 AGAAGGGAAAGGTTATTTGAGGACCGTCGA...CCTGCTTCAAACATGGA 1052

1048 AGAAGGGAAGGGTTATTTGAGGACCAG..GAGGCCAGCATCTAACATGGA 1095
    1053 TCCATACAGTGACTTCTATGATTGCTGAGACCAT..TCTATGGAA 1100

1096 CCCATACGTTGTTACTTCCATGATTGCTGAGACTACCATCCCTCT.T.GAA 1143
    1101 ACCTTAAATTACAAAG.TGGAGGCCAGT..TA.CAC.....GCGTGGTCG 1141

1144 ACC....AT....AAGCT..A..CCACTTGTACCACACAAAAAAC.T..T.A 1177
    1142 TGGGTGCTTTGCT.TTGGAGGCCAGCGCGTCACTGATAAGCTAATATGTATGT 1190

1178 TACTACATTG.TATTG....CAAC..CTTTGA.GAG.TCAT.TGT.TG. 1214
    1191 AAATGTGATGCCAAT.GTTTAAGTAGGTTGGTAACTTTGCTTTGGTTGTGTG 1239

1215 ....GT..T.CC..TCGTT..AG.AGATTGGT.TC.TTGGTTT..TTCTA 1248
    1240 GGTAGACCTGAACTTTGGTCAAACAATTTCCTCTTGCTATATGGATAT.A 1288
```

```
1249 G..GACATG.GCTTTG........TGT..TCTTG.T.TATGG.T.TCA 1279

1289 TATATATTTTGTATT.TGTTCTACTTG...TA.ATATG.G.CGAGGGCT 1331
     |||||||| ||||||| |||||          |||||| | |||| |
1280 CACGT.TGTTTGT.TTCT.TTCT.CTTGTTTTACTTATGTGTC.A...C. 1320

1332 TTAA.AAGACTCTCTT..TTACC..T.T..TATTTATTCCGTTG.TCGAA 1372
     ||||| ||| |||| | |||||   | |    ||| || ||||| |
1321 ..AATAATAATGTAATGGTTATCAGTATAATAATTATT..GTTGATTG.T 1365

1373 GATGTATT.CGACAAAT...TG..TTTAGAATG....T..T..TGAATAT 1408
     ||| ||||    |||||   ||   ||||  |     |   |   ||||||
1366 GAT.TATTAATAAAAATGTATGAATTGAAAATGCCCATGATAATGAATAT 1414

1409 GATAT.A...T.TCTTTGT.G 1423
     || ||| |   | ||||||||| |
1415 GA.ATGAGGGTGTCTTTGTAG 1434
```